

BATCH

RAW SEQUENCE LISTING                      DATE: 12/28/2000  
 PATENT APPLICATION: US/09/687,993      TIME: 15:50:02

Input Set : A:\687993.txt  
 Output Set: N:\CRF3\12282000\I687993.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Hu, Sylvia

7 (ii) TITLE OF INVENTION: Truncated Glial Cell Line-Derived Neurotrophin-3 Factor

10 (iii) NUMBER OF SEQUENCES: 50

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: AMGEN INC.

14 (B) STREET: 1840 DeHavilland Drive

15 (C) CITY: Thousand Oaks

16 (D) STATE: California

17 (E) COUNTRY: United States of America

18 (F) ZIP: 91320

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

26 (vi) CURRENT APPLICATION DATA:

C--&gt; 27 (A) APPLICATION NUMBER: US/09/687,993

C--&gt; 28 (B) FILING DATE: 13-Oct-2000

30 (vii) PRIOR APPLICATION DATA:

31 (A) APPLICATION NUMBER: US/08/535,681

32 (B) FILING DATE: 28-SEP-1995

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Curry, Daniel R.

36 (B) REGISTRATION NUMBER: 32,727

37 (C) REFERENCE/DOCKET NUMBER: A-357

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 805-447-8102

41 (B) TELEFAX: 805-499-8011

42 (C) TELEX:

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 402 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: protein

54 (ix) FEATURE:

55 (A) NAME/KEY: CDS

56 (B) LOCATION: 1..402

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

60 TCA CCA GAT AAA CAA ATG GCA GTG CTT CCT AGA AGA GAG CGG AAT CGG 48

61 Ser Pro Asp Lys Glu Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg

62 1 5 10 15 96

64 CAG GCT GCA GCT GCC AAC CCA GAG AAT TCC AGA GGA AAA GCT CGG ACA

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65 Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
66          20          25          30
68 GGC CAG AGG GGC AAA AAC CGG GGT TGT GTC TTA ACT GCA ATA CAT TTA      144
69 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
70          35          40          45
72 AAT GTC ACT GAC TTG GGT CTG GGC TAT GAA ACC AAG CAG GAA CTG ATT      192
73 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
74          50          55          60
76 TTT ACG TAC TGC AGC GGC TCT TGC GAT GCA GCT CAG ACA ACG TAC GAC      240
77 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
78 65          70          75          80
80 AAA ATA TTG AAA AAC ATA TCC AGA AAT AGA AGG CTG CTG AGT GAC AAA      288
81 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
82          85          90          95
84 GTA GGG CAG GCA TGT TGC AGA CCC ATC GCC TTT GAT GAT GAC CTG TCG      336
85 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
86          100          105          110
88 TTT TTA GAT GAT AAC CTG GTT TAC CAT ATT CTA AGA AAG CAT TCC GCT      384
89 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
90          115          120          125
92 AAA AGG TGT GGA TGT ATC      402
93 Lys Arg Cys Gly Cys Ile
94          130
96 (2) INFORMATION FOR SEQ ID NO: 2:
98   (i) SEQUENCE CHARACTERISTICS:
99       (A) LENGTH: 134 amino acids
100      (B) TYPE: amino acid
101      (D) TOPOLOGY: linear
103   (ii) MOLECULE TYPE: protein
105   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
107 Ser Pro Asp Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg
108 1          5          10          15
110 Gln Ala Ala Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg
111          20          25          30
113 Gly Gln Arg Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu
114          35          40          45
116 Asn Val Thr Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile
117          50          55          60
119 Phe Arg Tyr Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp
120 65          70          75          80
122 Lys Ile Leu Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys
123          85          90          95
125 Val Gly Gln Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser
126          100          105          110
128 Phe Leu Asp Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala
129          115          120          125
131 Lys Arg Cys Gly Cys Ile
132          130
134 (2) INFORMATION FOR SEQ ID NO: 3:

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136      (i) SEQUENCE CHARACTERISTICS:
137          (A) LENGTH: 4 amino acids
138          (B) TYPE: amino acid
139          (C) STRANDEDNESS: single
140          (D) TOPOLOGY: linear
142      (ii) MOLECULE TYPE: peptide
144      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
146      Lys Asn Arg Gly
147      1
149 (2) INFORMATION FOR SEQ ID NO: 4:
151      (i) SEQUENCE CHARACTERISTICS:
152          (A) LENGTH: 5 amino acids
153          (B) TYPE: amino acid
154          (C) STRANDEDNESS: single
155          (D) TOPOLOGY: linear
157      (ii) MOLECULE TYPE: peptide
159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
161      Gly Lys Asn Arg Gly
162      1      5
164 (2) INFORMATION FOR SEQ ID NO: 5:
166      (i) SEQUENCE CHARACTERISTICS:
167          (A) LENGTH: 6 amino acids
168          (B) TYPE: amino acid
169          (C) STRANDEDNESS: single
170          (D) TOPOLOGY: linear
172      (ii) MOLECULE TYPE: peptide
174      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
176      Arg Gly Lys Asn Arg Gly
177      1      5
179 (2) INFORMATION FOR SEQ ID NO: 6:
181      (i) SEQUENCE CHARACTERISTICS:
182          (A) LENGTH: 7 amino acids
183          (B) TYPE: amino acid
184          (C) STRANDEDNESS: single
185          (D) TOPOLOGY: linear
187      (ii) MOLECULE TYPE: peptide
189      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
191      Gln Arg Gly Lys Asn Arg Gly
192      1      5
194 (2) INFORMATION FOR SEQ ID NO: 7:
196      (i) SEQUENCE CHARACTERISTICS:
197          (A) LENGTH: 8 amino acids
198          (B) TYPE: amino acid
199          (C) STRANDEDNESS: single
200          (D) TOPOLOGY: linear
202      (ii) MOLECULE TYPE: peptide
204      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
206      Gly Gln Arg Gly Lys Asn Arg Gly
207      1      5

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209 (2) INFORMATION FOR SEQ ID NO: 8:
211   (i) SEQUENCE CHARACTERISTICS:
212       (A) LENGTH: 9 amino acids
213       (B) TYPE: amino acid
214       (C) STRANDEDNESS: single
215       (D) TOPOLOGY: linear
217   (ii) MOLECULE TYPE: peptide
219   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
221   Arg Gly Gln Arg Gly Lys Asn Arg Gly
222   1             5
224 (2) INFORMATION FOR SEQ ID NO: 9:
226   (i) SEQUENCE CHARACTERISTICS:
227       (A) LENGTH: 10 amino acids
228       (B) TYPE: amino acid
229       (C) STRANDEDNESS: single
230       (D) TOPOLOGY: linear
232   (ii) MOLECULE TYPE: peptide
234   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
236   Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
237   1             5             10
239 (2) INFORMATION FOR SEQ ID NO: 10:
241   (i) SEQUENCE CHARACTERISTICS:
242       (A) LENGTH: 11 amino acids
243       (B) TYPE: amino acid
244       (C) STRANDEDNESS: single
245       (D) TOPOLOGY: linear
247   (ii) MOLECULE TYPE: peptide
249   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
251   Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
252   1             5             10
254 (2) INFORMATION FOR SEQ ID NO: 11:
256   (i) SEQUENCE CHARACTERISTICS:
257       (A) LENGTH: 12 amino acids
258       (B) TYPE: amino acid
259       (C) STRANDEDNESS: single
260       (D) TOPOLOGY: linear
262   (ii) MOLECULE TYPE: peptide
264   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
266   Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
267   1             5             10
269 (2) INFORMATION FOR SEQ ID NO: 12:
271   (i) SEQUENCE CHARACTERISTICS:
272       (A) LENGTH: 13 amino acids
273       (B) TYPE: amino acid
274       (C) STRANDEDNESS: single
275       (D) TOPOLOGY: linear
277   (ii) MOLECULE TYPE: peptide
279   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
281   Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly

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282      1      5      10
284 (2) INFORMATION FOR SEQ ID NO: 13:
286   (i) SEQUENCE CHARACTERISTICS:
287       (A) LENGTH: 14 amino acids
288       (B) TYPE: amino acid
289       (C) STRANDEDNESS: single
290       (D) TOPOLOGY: linear
292   (ii) MOLECULE TYPE: peptide
294   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
296   Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
297      1      5      10
299 (2) INFORMATION FOR SEQ ID NO: 14:
301   (i) SEQUENCE CHARACTERISTICS:
302       (A) LENGTH: 15 amino acids
303       (B) TYPE: amino acid
304       (C) STRANDEDNESS: single
305       (D) TOPOLOGY: linear
307   (ii) MOLECULE TYPE: peptide
309   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
311   Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
312      1      5      10      15
314 (2) INFORMATION FOR SEQ ID NO: 15:
316   (i) SEQUENCE CHARACTERISTICS:
317       (A) LENGTH: 16 amino acids
318       (B) TYPE: amino acid
319       (C) STRANDEDNESS: single
320       (D) TOPOLOGY: linear
322   (ii) MOLECULE TYPE: peptide
324   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
326   Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg Gly
327      1      5      10      15
329 (2) INFORMATION FOR SEQ ID NO: 16:
331   (i) SEQUENCE CHARACTERISTICS:
332       (A) LENGTH: 17 amino acids
333       (B) TYPE: amino acid
334       (C) STRANDEDNESS: single
335       (D) TOPOLOGY: linear
337   (ii) MOLECULE TYPE: peptide
339   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
341   Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg Gly Lys Asn Arg
342      1      5      10      15
344   Gly
347 (2) INFORMATION FOR SEQ ID NO: 17:
349   (i) SEQUENCE CHARACTERISTICS:
350       (A) LENGTH: 18 amino acids
351       (B) TYPE: amino acid
352       (C) STRANDEDNESS: single
353       (D) TOPOLOGY: linear
355   (ii) MOLECULE TYPE: peptide

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VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/687,993

DATE: 12/28/2000  
TIME: 15:50:03

Input Set : A:\687993.txt  
Output Set: N:\CRF3\12282000\I687993.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:772 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39, Value={DNA}  
L:798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=40, Value={DNA}  
L:834 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:838 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:842 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:846 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:850 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:854 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:858 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41  
L:916 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:920 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:924 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:928 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:932 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:936 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:940 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43  
L:992 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45  
L:996 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45  
L:1000 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45  
L:1004 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45  
L:1008 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45  
L:1012 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45  
L:1016 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45